SEQUENCE LISTING

<110> Barany, Francis
Zebala, John
Nickerson, Deborah
Kaiser Jr., Robert J.
Hood, Leroy

<120> A THERMOSTABLE LIGASE MEDIATED DNA AMPLIFICATION SYSTEM
FOR THE DETECTION OF GENETIC DISEASES

<130> 19603/3641

<140>
<141>

<150> US 08/946,458
<151> 1997-10-07

<150> US 08/462,221
<151> 1995-06-05

<150> US 08/343,785
<151> 1994-11-22

<150> US 07/971,095
<151> 1992-11-02

<150> US 07/518,447
<151> 1990-05-03

<150> 09/480,515
<151> 2000-01-10

<160> 47

<170> PatentIn Ver. 2.1

<210> 1
<211> 2111
<212> DNA
<213> Thermus aquaticus ligase

<400> 1
tcggaatagg ggatgcgccc ctagtccaag ggaaagtata gcccaaggta cactagggcc 60
atgaccctgg aagaggcgag gaagcgggta aacgagttac gggacctcat ccgctaccac 120
aactaccgct actacgtcct ggcggacccg gagatctccg acgccgagta cgaccggctt 180
cttagggagc tcaaggagct tgaggagcgc ttccccgagc tcaaaagccc ggactccccc 240

```
acccttcagg tgggggcgag gcctttggag gccaccttcc gccccgtccg ccaccccacc 300
cgcatgtact ccttggacaa cgcctttaac cttgacgagc tcaaggcctt tgaggagcgg 360
atagaacggg ccctggggcg gaagggcccc ttcgcctaca ccgtggagca caaggtggac 420
gggctttccg tgaacctcta ctacgaggag ggggtcctgg tctacggggc caccgccggg 480
gacggggagg tgggggagga ggtcacccag aacctcctca ccatccccac catcccgagg 540
aggctcaagg gggtgccgga gcgcctcgag gtccgggggg aggtctacat gcccatagag 600
gccttcctcc ggctcaacga ggagctggag gagcgggggg agaggatctt caaaaaccct 660
aggaatgcgg cggcgggttc cttaaggcaa aaagaccccc gcatcaccgc caagcggggc 720
ctcagggcca ccttctacgc cttagggctt gggctggagg aggtggagag ggaaggggtg 780
gcgacccagt ttgccctcct ccactggctc aaggaaaaag gcttccccgt ggagcacggc 840
tacgcccggg ccgtgggggc ggaaggggtg gaggcggtct accaggactg gctcaagaag 900
cggcgggcgc ttccctttga ggcggacggg gtggtggtga agctggacga gcttgccctt 960
tggcgggagc tcggctacac cgcccgcgcc ccccggttcg ccatcgccta caagttcccc 1020
gccgaggaga aggagacccg gcttttggac gtggtcttcc aggtggggcg caccgggcgg 1080
gtgacccccg tggggatcct cgagcccgtc ttcctagagg gcagcgaggt ctcccgggtc 1140
accctgcaca acgagagcta catagaggag ttggacatcc gcatcgggga ctgggttttg 1200
gtgcacaagg cgggcggggt catccccgag gtcctccggg tcctcaagga gaggcgcacg 1260
ggggaggaaa ggcccattcg ctggcccgag acctgccccg agtgcggcca ccgcctcctc 1320
aaggagggga aggtccaccg ctgccccaac cccttgtgcc ccgccaagcg ctttgaggcc 1380
atccgccact tcgcctcccg caaggccatg gacatccagg gcctgggggа aaagctcatt 1440
gagaggcttt tggaaaaggg gctggtcaag gacgtggccg acctctaccg cttgagaaag 1500
gaagacctgg tgggcctgga gcgcatgggg gagaagagcg cccaaaacct cctccgcgag 1560
atagaggaga gcaagaaaag aggcctggag cgcctcctct acgccttggg gcttcccggg 1620
gtgggggagg tcttggcccg gaacctggcg gcccgcttcg ggaacatgga ccgcctcctc 1680
gaggccagcc tggaggagct cctggaggtg gaggaggtgg gggagctcac ggcgagggcc 1740
atcctggaga ccttgaagga ccccgccttc cgcgacctgg tacggaggct caaggaggcg 1800
ggggtggaga tggaggccaa ggagaagggc ggggaggccc ttaaagggct cacctccgtg 1860
atcaccgggg agctttcccg cccccgggaa gaggtgaagg ccctcctaag gcgcctcggg 1920
gccaaggtga cggactccgt gagccggaag acgagctacc tcgtggtggg ggagaacccg 1980
ggggagaacc cggggagcaa gctggagaag gccagggccc tcggggtccc caccctcacg 2040
gaggaggagc tctaccggct cctggaggcg cggacgggga agaaggcgga ggagctcgtc 2100
taaaggcttc c                                                      2111
```

<210> 2
<211> 676
<212> PRT
<213> Thermus aquaticus ligase

<400> 2

```
Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp Leu
  1               5                  10                  15

Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro Glu Ile
             20                  25                  30

Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
         35                  40                  45
```

Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Leu Gln Val
50 55 60

Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
65 70 75 80

Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn Leu Asp Glu Leu Lys Ala
85 90 95

Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Ala
100 105 110

Tyr Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
115 120 125

Glu Glu Gly Val Leu Val Tyr Gly Ala Thr Arg Gly Asp Gly Glu Val
130 135 140

Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
145 150 155 160

Arg Leu Lys Gly Val Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr
165 170 175

Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg
180 185 190

Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
195 200 205

Arg Gln Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr
210 215 220

Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
225 230 235 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe Pro
245 250 255

Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val Glu Ala
260 265 270

Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro Phe Glu Ala
275 280 285

Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu Trp Arg Glu Leu
290 295 300

```
Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro
305                 310                 315                 320

Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp Val Val Phe Gln Val Gly
                325                 330                 335

Arg Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Leu
            340                 345                 350

Glu Gly Ser Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile
        355                 360                 365

Glu Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala
    370                 375                 380

Gly Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr
385                 390                 395                 400

Gly Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly
                405                 410                 415

His Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu
            420                 425                 430

Cys Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys
        435                 440                 445

Ala Met Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu
    450                 455                 460

Glu Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
465                 470                 475                 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln Asn
                485                 490                 495

Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu Arg Leu
            500                 505                 510

Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn
        515                 520                 525

Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu Glu Ala Ser Leu
    530                 535                 540

Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala
545                 550                 555                 560
```

Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg
565 570 575

Leu Lys Glu Ala Gly Val Glu Met Glu Ala Lys Glu Lys Gly Gly Glu
580 585 590

Ala Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro
595 600 605

Arg Glu Glu Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr
610 615 620

Asp Ser Val Ser Arg Lys Thr Ser Tyr Leu Val Val Gly Glu Asn Pro
625 630 635 640

Gly Ser Lys Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr
645 650 655

Glu Glu Glu Leu Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala
660 665 670

Glu Glu Leu Val
675

<210> 3
<211> 7
<212> PRT
<213> Thermus aquaticus

<400> 3
Asp Ala Glu Tyr Asp Arg Leu
1 5

<210> 4
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate Probe

<220>
<221> unsure
<222> (3)

<223> Y at position 3 in this sequence can be either c
or t

<220>
<221> unsure
<222> (12)
<223> Y at position 12 in this sequence can be either c
or t

<220>
<221> unsure
<222> (15)
<223> Y at position 15 in this sequence can be either c
or t

<220>
<221> unsure
<222> (19)
<223> Y at position 19 in this sequence can be either c
or t

<220>
<221> unsure
<222> (6)
<223> N at position 6 in this sequence can be either a,
g, c, or t

<220>
<221> unsure
<222> (18)
<223> N at position 18 in this sequence can be either a,
g, c, or t

<220>
<221> unsure
<222> (9)
<223> R at position 9 in this sequence can be either g
or a

<220>
<221> unsure
<222> (16)
<223> M at position 16 in this sequence can be either c
or a

<400> 4
gaygcngart aygaymgnyt 20

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo Primer

<400> 5
agcggataac aatttcacac agga 24

<210> 6
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: pTZ18R

<400> 6
ggctcgtatg ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga 60
ccatgattac gaatttaata cgactcacta tagggaattc gagctcggta ccccaaggta 120
cactagggcc 130

<210> 7
<211> 2051
<212> DNA
<213> Thermus aquaticus ligase

<400> 7
atgaccctgg aagaggcgag gaagcgggta aacgagttac gggacctcat ccgctaccac 60
aactaccgct actacgtcct ggcggacccg gagatctccg acgccgagta cgaccggctt 120
cttagggagc tcaaggagct tgaggagcgc ttccccgagc tcaaaagccc ggactccccc 180
acccttcagg tgggggcgag gcctttggag gccaccttcc gccccgtccg ccaccccacc 240
cgcatgtact ccttggacaa cgcctttaac cttgacgagc tcaaggcctt tgaggagcgg 300
atagaacggg ccctggggcg gaagggcccc ttcgcctaca ccgtggagca caaggtggac 360
gggctttccg tgaacctcta ctacgaggag ggggtcctgg tctacggggc caccgccggg 420
gacggggagg tgggggagga ggtcacccag aacctcctca ccatccccac catcccgagg 480
aggctcaagg gggtgccgga gcgcctcgag gtccgggggg aggtctacat gcccatagag 540
gccttcctcc ggctcaacga ggagctggag gagcgggggg agaggatctt caaaaaccct 600
aggaatgcgg cggcgggttc cttaaggcaa aaagaccccc gcatcaccgc caagcggggc 660
ctcagggcca ccttctacgc cttagggctt gggctggagg aggtggagag ggaaggggtg 720
gcgacccagt ttgccctcct ccactggctc aaggaaaaag gcttccccgt ggagcacggc 780
tacgcccggg ccgtgggggc ggaaggggtg gaggcggtct accaggactg gctcaagaag 840
cggcgggcgc ttccctttga ggcggacggg gtggtggtga agctggacga gcttgccctt 900

tggcgggagc tcggctacac cgcccgcgcc ccccggttcg ccatcgccta caagttcccc 960
gccgaggaga aggagacccg gcttttggac gtggtcttcc aggtgggccg caccgggcgg 1020
gtgacccccg tggggatcct cgagcccgtc ttcctagagg gcagcgaggt ctcccgggtc 1080
accctgcaca acgagagcta catagaggag ttggacatcc gcatcgggga ctgggttttg 1140
gtgcacaagg cgggcggggt catccccgag gtcctccggg tcctcaagga gaggcgcacg 1200
ggggaggaaa ggcccattcg ctggcccgag acctgccccg agtgcggcca ccgcctcctc 1260
aaggagggga aggtccaccg ctgccccaac cccttgtgcc ccgccaagcg ctttgaggcc 1320
atccgccact tcgcctcccg caaggccatg gacatccagg gcctggggga aaagctcatt 1380
gagaggcttt tggaaaaggg gctggtcaag gacgtggccg acctctaccg cttgagaaag 1440
gaagacctgg tgggcctgga gcgcatgggg gagaagagcg cccaaaacct cctccgcgag 1500
atagaggaga gcaagaaaag aggcctggag cgcctcctct acgccttggg gcttcccggg 1560
gtgggggagg tcttggcccg gaacctggcg gcccgcttcg ggaacatgga ccgcctcctc 1620
gaggccagcc tggaggagct cctggaggtg gaggaggtgg gggagctcac ggcgagggcc 1680
atcctggaga ccttgaagga ccccgccttc cgcgacctgg tacggaggct caaggaggcg 1740
ggggtggaga tggaggccaa ggagaagggc ggggaggccc ttaaagggct cacctccgtg 1800
atcaccgggg agctttcccg cccccgggaa gaggtgaagg ccctcctaag gcgcctcggg 1860
gccaaggtga cggactccgt gagccggaag acgagctacc tcgtggtggg ggagaacccg 1920
ggggagaacc cggggagcaa gctggagaag gccagggccc tcggggtccc caccctcacg 1980
gaggaggagc tctaccggct cctggaggcg cggacgggga agaaggcgga ggagctcgtc 2040
taaaggcttc c 2051

<210> 8
<211> 676
<212> PRT
<213> Thermus aquaticus ligase

<400> 8
Met Thr Leu Glu Glu Ala Arg Lys Arg Val Asn Glu Leu Arg Asp Leu
1 5 10 15

Ile Arg Tyr His Asn Tyr Arg Tyr Tyr Val Leu Ala Asp Pro Glu Ile
20 25 30

Ser Asp Ala Glu Tyr Asp Arg Leu Leu Arg Glu Leu Lys Glu Leu Glu
35 40 45

Glu Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Leu Gln Val
50 55 60

Gly Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr
65 70 75 80

Arg Met Tyr Ser Leu Asp Asn Ala Phe Asn Leu Asp Glu Leu Lys Ala
85 90 95

Phe Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Ala
100 105 110

Tyr Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr
115 120 125

Glu Glu Gly Val Leu Val Tyr Gly Ala Thr Arg Gly Asp Gly Glu Val
130 135 140

Gly Glu Glu Val Thr Gln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg
145 150 155 160

Arg Leu Lys Gly Val Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr
165 170 175

Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg
180 185 190

Gly Glu Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
195 200 205

Arg Gln Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr
210 215 220

Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Val Glu Arg Glu Gly Val
225 230 235 240

Ala Thr Gln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Gly Phe Pro
245 250 255

Val Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val Glu Ala
260 265 270

Val Tyr Gln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro Phe Glu Ala
275 280 285

Asp Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu Trp Arg Glu Leu
290 295 300

Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro
305 310 315 320

Ala Glu Glu Lys Glu Thr Arg Leu Leu Asp Val Val Phe Gln Val Gly
325 330 335

Arg Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Leu
340 345 350

Glu Gly Ser Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile
355 360 365

Glu Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala
370 375 380

Gly Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr
385 390 395 400

Gly Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly
405 410 415

His Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu
420 425 430

Cys Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe Ala Ser Arg Lys
435 440 445

Ala Met Asp Ile Gln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu
450 455 460

Glu Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys
465 470 475 480

Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln Asn
485 490 495

Leu Leu Arg Gln Ile Glu Glu Ser Lys Lys Arg Gly Leu Glu Arg Leu
500 505 510

Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn
515 520 525

Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu Glu Ala Ser Leu
530 535 540

Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala
545 550 555 560

Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg
565 570 575

Leu Lys Glu Ala Gly Val Glu Met Glu Ala Lys Glu Lys Gly Gly Glu
580 585 590

Ala Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro
595 600 605

Arg Glu Glu Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr
610 615 620

Asp Ser Val Ser Arg Lys Thr Ser Tyr Leu Val Val Gly Glu Asn Pro
625 630 635 640

Gly Ser Lys Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr
645 650 655

Glu Glu Glu Leu Tyr Arg Leu Leu Glu Ala Arg Thr Gly Lys Lys Ala
660 665 670

Glu Glu Leu Val
675

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 9
ctggcttatc gaaattaat 19

<210> 10
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 10
ccagggtcat tttattttct ccatgtacaa at 32

<210> 11
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 11
catggagaaa ataaaatgac cctggaagag gcg 33

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 12
aagccggtcg tactcggc 18

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 13
gtttttcatg gtgcacctga cgcctgg 27

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 14
gtttcatggt gcacctgacg cctct 25

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 15
gtcatggtgc acctgacgcc tca 23

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 16
ggagaagtct gccgttactg cc 22

<210> 17
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaA-globin
forward primer

<400> 17
gacaccatgg tgcacctgac tcctgaggag aagtctgccg ttactgccct g 51

<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaA-globin
reverse primer

<400> 18
ctgtggtacc acgtggactg aggactcctc ttcagacggc aatgacggga c 51

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
tggtaccacg tggactgagg ac 22

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
tcctcttcag acggcaatga cgtc 24

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21
acctcttcag acggcaatcg cgtttc 26

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 22
ccctcttcag acggcaatcg cgtttttc 28

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaA-globin

<400> 23
Met Val His Leu Thr Pro Glu Glu Lys Ser Ala Val Thr Ala Leu
1 5 10 15

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaS-globin

<400> 24
Met Val His Leu Thr Pro Val Glu Lys Ser Ala Val Thr Ala Leu
1 5 10 15

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: beta-globin amplification primer

<400> 25
caacttcatc cacgttcacc ttgcc 25

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: beta-globin amplification primer

<400> 26
agggcaggag ccagggctgg gg 22

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Alpha1 - antitrypsin amplification primer

<400> 27
tcagccttac aacgtgtctc tgctt 25

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Alpha1 - antitrypsin amplification primer

<400> 28
gtatggcctc taaaaacatg gcccc 25

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cystic fibrosis amplification primer

<400> 29
cagtggaaga atggcattct gtt 23

<210> 30

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cystic fibrosis amplification primer

<400> 30
ggcatgcttt gatgacgctt ctg 23

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaA-globin primer

<400> 31
atggtgcacc tgactcctga 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo primer

<400> 32
ggagaagtct gccgttactg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: betaS-globin primer

<400> 33
atggtgcacc tgactcctgt 20

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Alpha1 -
antitrypsin(M) primer

<400> 34
ggctgtgctg accatcgacg 20

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo primer

<400> 35
agaaagggac tgaagctgct 20

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Alpha1
antitrypsin(Z) primer

<400> 36
ggctgtgctg accatcgaca 20

<210> 37
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cystic
fibrosis (non-508) primer

<400> 37
attaaagaaa atatcatctt 20

<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 38
tggtgtttcc tatgatgaat 20

<210> 39
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cystic
fibrosis (508) primer

<400> 39
accattaaag aaaatatcat 20

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 40
gtcatggtgc acctgactcc tga 23

<210> 41
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 41
gtttcatggt gcacctgact cctgt 25

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 42
gtttttcatg gtgcacctga ctcctgg 27

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 43
ctgcagtaac ggcagacttc tcct 24

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 44
ctttgcagta acggcagact tctcca 26

<210> 45
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 45
cttttgcag taacggcaga cttctccc 28

<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 46
ggagaagtct gccgttactg cc 22

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 47
caggagtcag gtgcaccatg gt 22